************************ (MT)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat May 13 09:29:15 2000; MasPar time 3.98 Seconds 267.936 Million cell updates/sec

Tabular output not generated.

Title:

Description:
Perfect Score:
Sequence: >US-09-331-631-1
(29-73) from US09331631.pep (2 of 5)
361
1 SEFDRQEYEECKRQCMQLETSGQMRRCVSQCDKRFEEDIDWSKYD 45

Scoring table: PAM 150 Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq35 1:geneseqp

Statistics: Mean 24.753; Variance 88.190; scale 0.281

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 3 3 3 4 4 4 5 5 6 6 7 7 8 7 11 12 22 22 22 22 23 23 24 24 24 25 26 26 27 27 27 28 28 28 28 28 28 28 28 28 28 28 28 28	Result No.
361 259 109 109 97 97 77 77 77 77 77 77 77	Score
100.0 71.7 26.9 26.9 26.3 27.3 27.3 27.3 21.3 21.3 21.3 21.3 21.3 21.3 21.3 21	Query Match
666 6666 5595 5595 5666 2318 2318 2318 2318 2444 444 444 448 448 448 448 524 524 524 524 524 524 524 524 524 524	Length
	DB
W W 62828 W 62828 W 62832 W 62832 W 62832 R 201831 R 201831 R 20183 R 20183	ID
Macadamia integrifolia Macadamia integrifolia Macadamia integrifolia Macadamia integrifolia Macadamia integrifolia Macadamia integrifolia Gossypium hirsutum ant Theobroma cacao antimi Sequence encoded by 67 Human TsP1 protein. Human thrombospondin 1 Human concatamerised Thuman concatamerised Thuman truncated SBP2 Maize Id gene product. G. max truncated SBP1 G. max SBP2 protein. G. max SBP1 protein. G. max SBP1 protein. Human 5' EST secreted HE4 epididymis-specifi Human HE4 protein. Sequence encoded by a Zea mays antimicrobial Human strovirus serot P. falciparum Proj3.	Description
2.58e-30 9.96e-19 1.88e-01 1.88e-01 1.88e-01 2.93e-01 2.93e-01 2.93e-01 1.39e+01 1.39e+01 1.39e+01 1.39e+01 1.39e+01 1.39e+01 3.18e+	Pred. No.

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18.3	18.3	18.3	18.3	18.3	18.3	18.3	18.3	18.3	18.6	18.6	18.6	18.6	18.8	18.8	18.8	19.1	19.1	19.4	19.4	19.4	19.7
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Y04137	Y04136	R15299	W80302	R81473	W54097	R57061	W07823	W08904	W55960	Y04841	R47557	Y04837	W44119	R85870	W30622	R21079	W62836	W06576	R91311	Y11721	W22475
3 protein	Human slit 3 mature pr	•	A thermophilic ligase	Thermus aquaticus DNA	Homo sapiens B223 sequ	P. aeruginosa mucA.	Cyclic corticotrophin	(Cyclo 30-33)[D-Phe12,	Human transient recept	Mycobacterium species	ILTV thymidine kinase.	Mycobacterium species	Human type C lectin.	WD-40 domain-contg. Mu	Arabidopsis enhanced d	Antimicrobial maize pe	Zea mays antimicrobial	Neisseria polyglycosyl	N. gonorrhoeae glycosy	Human 5' EST secreted	Plasmodium var-7.
1.29e+02	1.29e+02	1.29e+02	1.29e+02	1.29e+02	1.29e+02	1.29e+02	1.29e+02	1.29e+02	1.06e+02	1.06e+02	1.06e+02	1.06e+02	8.70e+01	8.70e+01	8.70e+01	7.13e+01	7.13e+01	5.83e+01	5.83e+01	5.83e+01	4.77e+01

ALIGNMENTS

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SUL	:	Query Best I Matche		SUI
W62828 standard; Protein; 666 AA. W62828; 27-00T-1998 (first entry) Macadamia integrifolia antimicrobial protein. Macadamia integrifolia. Macadamia integrifolia. Macadamia integrifolia. Key Location/Qualifiers Key 1. 28 Peptide /note= "signal peptide"	29 SEFDRQEYEECKRQCMQLETSGQMRRCVSQCDKRFEEDIDWSKYD 73	Query Match 100.0%; Score 361; DB 1; Length 666; Best Local Similarity 100.0%; Pred. No. 2.58e-30; Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps	rst entry) ifolia ant ifolia; inf ifolia. Location/C 128 /note= "si 29666 /note= "ma 004275. CCENT TROP r KC, Gree 2. KC, Gree 2. Location/C 128 Location/C 2. Lo	T W62829 standard; Protein; 666 AA.

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antimicrobial protein; infestation;
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W62832 standard; Protein; 9
W62832;
27-OCT-1998 (first entry)
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The sequence is that of an antimicrobial protein which can be sequenced in the control of the sequence of the control of the sequence of the control o
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Novel anti-microbial protein from e.g. Macadamia integrifol useful for controlling microbial infestations of plants or Claim 1; Page 34-36; 96pp; English.

The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and man
                                                                      02-JUL-1998
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BOWER NI, Goulter KC, Green JL, Manners JM, Mar
WPI; 98-377279/32.
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22-DEC-1997; AU0874.
20-DEC-1996; AU-004275.
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Local Similarity 100.0%;
hes 32; Conservative
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COOP RES CENT TROPICAL PLANT PATHOLOGY.
II, Goulter KC, Green JL, Manners JM, Marcus
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/note= "signal peptide"
29. .666
/note= "mature protein"
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Pred. No. 2.58e-30;
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07-JUN-1991; GB-013016.

11-JUN-1990; GB-013016.

(MRSC) MARS UK LTD

Spencer ME, Hodge R, Deakin E/

WPI; 92-024418/03.

N-PDDB; Q20377.
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Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;

WPI; 98-377279/32.

Novel anti-microbial protein from e.g. Macadamia integrifolia -
useful for controlling microbial infestations of plants or mammals

Claim 1; Page 49-51; 96pp; English.

The sequence is that of an antimicrobial protein which can

be used to control microbial infestations in plants and mammalian
                                                                   expression vectors
Claim 4; Fig 2; 59pp;
The inventors claim a
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22-DEC-1997; AU0874.
20-DEC-1996; AU-004275.
(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
BOWER NI, Goulter KC, Green JL, Manners JM, Mar
WPI; 98-377279/32.
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Sequence encoded by 67 kD T.
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                                                                                                                                                               beans and produced in large
                                                                                                                                                                                                          Recombinant cocoa proteins -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Theobroma cacao.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cocoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antimicrobial protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Theobroma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          be used to control microbial infestations animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9119801-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        be used to control microbial infestations in plants and mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel anti-microbial protein from e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9827805-A1.
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20-DEC-1996; AU-004275.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 RQQYEQCQRRCESEATEEREQEQCEQRCEREYKEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 YEECQQECRQQEER-QQPQCQQRCLKRFEQE 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           flavour; vicilin; seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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larity 31.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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45.2%;
                                                                   English.
67 kD and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infestation; co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              566
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Pred. No. 1.
11; Mismatc

    are responsible
quantities using

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Pred. No. 1.26e-02;
6; Mismatches 10
                                                                                                                                                                                                                                                                                                                 EA, Ashton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cacao protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           storage
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                                                                      31
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                                                                      kυ T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         control
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                                                                                                                                                                                                                                                                                                                 S
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1.88e-01
                                                                      cacao
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                                                                                                                                                                      for flavour in yeast and bacte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
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                                                                   protein,
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Matches 1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                          21-JAN-1998.
16-JUL-1997; 112154.
16-JUL-1996; US-680845.
(MIXS/) MIXSON A J.
Mixson AJ;
                                        R40823 stand
R40823;
R40823;
03-MAR-1994
                                                                                                                                                                                                                                           Claim 9; Page 6; 47pp; English.

This sequence represents the thrombospondin gene TSP1 which is used in a method to produce a cationic vehicle consisting of a cationic liposome:DNA complex where the DNA encodes an anti-angiogenic peptide or tumour suppressor protein. Such complexes are used for treatment of neoplastic and metabolic diseases especially for gene therapy of tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 7
W40287 standard; Protein;
W40287;
18-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragments, and encoding DNAs. The 47 kD and 31 kD proteins are derived from the 67 kD precursor. T. cacco protein CDNA was detected in a cDNA library prepared from immature cocoa beans RNA using a probe based on the AA sequence of a CNBr peptide common to the 47 kD and 31 kD polypeptides. Homology searches revealed close homologies between the 67 kD polypeptide and the vicilins, which are
Human thrombospondin hTSP-1; platelet glyo inhibitor; solid tumo
                                                                                                                                                                                                                                                                                                                                                   Complexes of DNA encoding anti-angiogenic peptide - with cationic liposome(s) or cationic polymer, useful for, e.g. gene therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seed storage proteins.
Sequence 566 AA;
                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; V10493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 metabolic disease; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human TSP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             liposome;
                                                                                                                                                     116 SSVQTRTCHIQECDKRFKQDGGWS 139
                                                                                                                             48
                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \omega
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 RQQYEQCQRRCESEATEEREQEQCEQRCEREYKEQ
                                                                                                                           TSGQMRRC-VSQCDKRFEEDIDWS
                                                                                                                                                                                                                                                                                                                                                                                             98-078839/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thrombospondin; anti-angiogenic; cationic vehicle; gene therapy; ome; DNA complex; tumour suppressor protein; treatment; neoplastic;
                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
11; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.9%;
llarity 31.4%;
Conservative
                                       (first entry)
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "encoded by CGG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=
199. .21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
glycoprotein; angiogenesis; neovascularisation;
tumour; skin cancer; angiogenic dysfunction;
                                                                    protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note=
                                                                                                                                                                                              26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21= anti-angiogenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-angiogenic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anti-angiogenic
                                                                     239
                                                                                                                                                                             Score 95; DB 1; Len
Pred. No. 2.93e-01;
'w'smatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 97; DB 1;
Pred. No. 1.88e-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide
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                                                                                                                                                                                                           Length 218;
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Best Local S
Matches 1
  Query Match 26.3% Best Local Similarity 50.0% Matches 12; Conservative
                                                   This protein sequence represents a concatamer of thrombospondin TSP which is used in a method to produce a cationic vehicle consisting of a cationic liposome.DNA complex where the DNA encodes an anti-angiogenic peptide or tumour suppressor protein. Such complexe used for treatment of neoplastic and metabolic diseases especially gene therapy of tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W40288
W40288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-SEP-1993.
22-FEB-1993; U01652.
24-FEB-1992; US-841656.
(NOUN ) UNIV NORTHWESTERN.
BOUCK NP, Frazier WA, Good DJ, Polverini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Certain fragments of thrombospondin, a glycoprotein found in the alpha granules of platelets, can inhibit vascularisation. Peptid derived from the hTSP sequence are useful for inhibiting neovascularisation, esp. In solid tumours such as melanomas. The inhibitory peptides can also be used in other diseases involving angiogenic dysfunction. See R40824-R40830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 93 288118/36.
Compsn. for inhibiting angiogenesis inhibitor comprising a peptide capal
                                                                                                                                     tumours .

Claim 9; Page 6-7; 47pp; English.
                                                                                                                                                                  Complexes of DNA encoding anti-angiogenic peptide - with cationic liposome(s) or cationic polymer, useful for, e.g. gene therapy of
                                                                                                                                                                                             N-PSDB; V10494
                                                                                                                                                                                                                                                                                                                                                    /note=
Misc_difference 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human concatamerised TSP1 protein.
TSP1; thrombospondin; anti-angiogenic; cationic vehicle; gene therapy;
liposome; DNA complex; tumour suppressor protein; treatment; neoplasti
                                                                                                                                                                                                                                                                                    EP-819758-A2.
                                                                                                                                                                                                                                                                                                              Region
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Misc_difference 160
                                                                                                                                                                                                                                                                                                                                                                                                                                            metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vascularisation
Claim 10; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
W09316716-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       melanoma; diabetic retinopathy; psoriasis; neovascular glaucoma; Kaposi's sarcoma; inflammation; retrolental fibroplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-AUG-1998
                                                                                                                                                                                                                      Mixson AJ;
                                                                                                                                                                                                                                               16-JUL-1997; 112154.
16-JUL-1996; US-680845.
                                                                                                                                                                                                                                                                        21-JAN-1998.
                                                                                                                                                                                                                                  (MIXS/) MIXSON A J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 SSVQTRTCHIQECDKRFKQDGGWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSGQMRRC-VSQCDKRFEEDIDWS
                                                                                                                                                                                                           98-078839/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 12; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                          disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 41-42; 51pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                       /note=
383
                                                                                                                                                                                                                                                                                                            /note=
223. .2
                                                                                                                                                                                                                                                                                                   /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                           concatamer; tumour.
              26.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                            encoded .227
                                                                                                                                                                                                                                                                                                                                                                           "encoded by CGG"
                                                                                                                                                                                                                                                                                                                                                   "encoded
                                                                                                                                                                                                                                                                                                intervening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     441
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   Score
Pred.
4; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Å
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                                                                                                                                                                                                                                                                                                                          by ccc."
                                                                                                                                                                                                                                                                                                                                                  by GAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
               95;
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DB 1; 2.93e-01; 7;
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2.93e-01;
2.93e-7;
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e of inhibiting
                           Length 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 239;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                          This sequence represents a novel sucrose binding protein, SBP2 isolated from Glycine max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which has a modified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wild-type SBP. The products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              altering the induction of flowering in plants Claim 7; Fig 3 and Fig 5; 58pp; English.

The Id gene controls flower evocation in maize plants. maize nucleic acid is similar to that of genes encoding finger regulatory proteins in animals.

Transposons Ac and Ds constitute a family of related trelements present in maize. A derivative of Ds, Ds2, can be present in maize. A derivative of Ds, Ds2, can be present in maize.
                                                                                                                                                                                                                                                                                                                        WPI; 99-070155/06.

New modified plant sucrose binding proteins - use transgenic plants which can have enhanced or decruptake activity in developing seeds Claim 7; Page 39-40; 58pp; English.

This sequence represents a novel sucrose binding the contraction of 
       desirable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chao WS, Grimes HD; WPI; 99-070155/06.
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21-MAY-1998; U10465
22-MAY-1997; US-047!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycine max. WO9853086-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seed; carbohydrate content;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G. max truncated SBP2 protein.
SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W9034
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WPI; 96-49762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-1996.
15-MAR-1996; U03466.
16-MAR-1995; US-406186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays
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[UNIW] UNIV WASHINGTON STATE RES FOUND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ements present in maize. A derivative of Ds, Ds2, can I produce a new mutant of the Id gene. The Ds2 (in the I active Ac) is excised from a nearby gene on chromosome d inserted into the Id gene to produce id*.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEKRWCCERCGKPYAVQSDW
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flower evocation; zinc-finger regulatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
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where it is an advantage to increase the carbohydrate
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. 1.39e+01;
. Thes 7;
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18-FEB-1998: U03161.
30-DEC-1997: US-000640.
20-FEB-1997: US-00104.
(COLD-) COLD SPRING HARBOR LA
Chao WS, Grimes HD;
WPI; 99-070155/06.
New modified plant sucrose binding protein
transgenic plants which can have enhanced
uptake activity in developing seeds
                                                                                                                             26-NOV-1998.
21-MAY-1998; U10465.
22-MAY-1997; US-047568.
(UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                Glycine max. WO9853086-A1.
                                                                                                                                                                                                                                                                        24-MAY-1999 (first entry)
G. max truncated SBP1 protein.
SBP1; sucrose binding protein; SBP2; seed; carbohydrate content; soybean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ind gene controlling floral induction in maize - useful to create transgenic plants with earlier, delayed or inhibited floral induction e.g. to extend geographical range of crops Claim 5; Fig 3; 68pp; English.

The maize Id gene controls floral induction and is useful in the production of transgenic plants with altered floral induction times, i.e. earlier, delayed or inhibited floral induction. The Id gene and zinc-finger regulatory regions are useful to identify these genes in maize and isolate similar genes in other plants. The polypeptides and antibodies are also useful in Id detection e.g. to locate activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the seed (e.g. where the seed is the primary plant material harveste such as soybean). In contrast, decreased sucrose uptake activity in seeds might be desirable where the vegetative material of the plant is harvested. The SBP regulatory regions confer specific or enhanced expression in developing seeds and so may be used to express any
                                                                                                                                                                                                                                                                                                                                                                                  W90340
                                                                                                                                                                                                                                                                                                                                                                                                      W90340
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WPI; 98-467564/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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WO9837201-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 GEKRWCCERCGKPYAVQSDW
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                                                                                                                                                                                                                                                                                                                                                                                                      protein;
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6; M
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Pred.
6; M
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                                                                                                                                                                                                                                                                                                      SBP2; sucrose uptake; transgenic plant;
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1. No. 1.39e+01;
Mismatches 7
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                                                         proteins -
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1.39e+01;
                                     or
                                     decreased
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The products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds may be consisted the seed (e.g. where it is an advantage to increase the carbohydrate content of the seed (e.g. where the seed is the primary plant material harvested, contrast, decreased sucrose uptake activity in seeds and so may be used to express any in developing seeds and so may be used to express any
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This sequence represents a novel sucrose binding protein, SBP1 isolated from Glycine max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which has a commodified amino acid sequence compared to a corresponding which has a commodified amino acid sequence compared to a corresponding which type SBP, and where expression of the modified SBP in a yeast assay system confers cenhanced sucrose uptake compared to the corresponding which type SBP.

CC The products of the invention can be used for producing transgenic plants which have modified sucrose uptake activity, particularly in developing seeds. Enhanced sucrose uptake activity in developing seeds. Enhanced sucrose uptake activity in developing seeds may be constantly where it is an advantage to increase the carbohydrate content of the seed (e.g. where the seed is the primary plant material harvested. Such as soybean). In contrast, decreased sucrose uptake activity in seeds might be desirable where the vegetative material of the plant is cardinated. The SBP regulatory regions confer specific or enhanced transgene in developing seeds and so may be used to express any confers and contract and contract
                                                                                                                                                                       Query Match
Best Local S
Matches 1
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Best Local Similarity
Matches 12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAY-1998; U10465.
22-MAY-1997; US-047568.
(UNIW) FUNIV WASHINGTON STATE RES FOUND.
Chao WS, Grimes HD;
WPI; 99-070155/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New modified plant sucrose binding proteins - used to develop transgenic plants which can have enhanced or decreased sucrose uptake activity in developing seeds uptake activity in developing seeds Claim 13b; Page 37-38; 58pp; English.
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                                                                                 42 CKHQCQQQRQYTESDKRTCLQQCD
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CKROCMQL-E-TSGQMRRCVSQCD
                                                                                                                                                                       Similarity
11; Conser
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Pred. No. 1.39e+01;
6; Mismatches 6;
                                                                                                                                                                                                                  Score 77; DB 1;
Pred. No. 1.39e+01
                                                                                                                                                                            6
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                                                                                                                                                                            Mismatches
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                                                                                                                                                                        Query Match 21.3%;
Best Local Similarity 44.4%;
Matches 12; Conservative
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WPI; 99-070155/06.

New modified plant sucrose binding proteins - used to develop transgenic plants which can have enhanced or decreased sucrose uptake activity in developing seeds
Disclosure; Page 34-36; 58pp; English.

This sequence represents a novel sucrose binding protein, SBPl isolated from Glycine max. This protein is used in a method resulting in the production of a modified plant sucrose binding protein (SBP) which has a modified amino acid sequence compared to a corresponding wild-type SBP, and where expression of the modified SBP in a yeast assay system confers enhanced sucrose uptake compared to the corresponding wild-type SBP.

The products of the invention can be used for producing transgenic plants
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W90339 standard; protein; 524 AA.

W90339;

24 MAY-1999 (first entry)

G. max SBP1 protein.
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WO9853086-A1.
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21-MAY-1998; U10465.
22-MAY-1997; US-047568
39 CKRQCMQLE--TSGQMRRCVSQCDKRF
                                                                                    43 CKHQCQQQQYTEGDKRVCLQSCD-RY 68
                                                                                                                                                                                                                                                                                                                                                              524 AA;
                                                                                                                                                                                                                  Score 77; DB 1;
Pred. No. 1.39e+01
63
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